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Sequence Listing was accepted.
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217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2008; month=2; day=19; hr=12; min=44; sec=17; ms=821; ]
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Validated By CRFValidator v 1.0.3

Application No: 10576439   Version No: 1.0

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Finished: 2008-02-08 16:44:25.156
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Total Errors: 0
No. of SeqIDs Defined: 7
Actual SeqID Count: 7

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<110>   Theratechnologies Inc.
        Lussier, Bruno
        Vachon, Luc
        Allas, Soraya
        Abribat, Thierry

<120>   Selection and treatment of patients suffering from wasting

<130>   09555.0151USWO

<140>   10576439
<141>   2008-02-08

<150>   PCT/CA2004/001843
<151>   2004-10-20

<150>   60/512,198
<151>   2003-10-20

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<223>   GRF peptide

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<223>   Xaa = Tyr or His

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<223>   Xaa = Val or Ala

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<223>   Xaa = Asn or Ser

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<223>   Xaa = Val or Ile

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<222>   (15)..(15)
<223>   Xaa = Ala or Gly


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<223>   Xaa = Gln or His


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<223>   Xaa = Met or Ile or Nle


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<221>   VARIANT
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<223>   Xaa = Ser or Asn


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<222>   (30)..(30)
<223>   Xaa = amino acid sequence of 1 up to 15 residues or is a bond


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Xaa Xaa Asp Ala Ile Phe Tyr Xaa Ser Tyr Arg Lys Xaa Leu Xaa Gln
1               5                   10                  15


Leu Xaa Ala Arg Lys Leu Leu Xaa Xaa Ile Xaa Xaa Arg Xaa
            20                  25                  30



<210>   2
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<212>   PRT
<213>   Homo sapiens



<220>
<221>   MISC_FEATURE
<222>   (44)..(44)
<223>   Leu residue is capped with an unsubstituted amide moiety


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Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
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```
1               5                  10                    15

Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
            20                    25              30


Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu
        35              40


<210>   3
<211>   44
<212>   PRT
<213>   Artificial sequence

<220>
<223>   Amino acid sequence of human GRF

<400>   3

Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
1               5                  10                    15


Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
            20                    25              30


Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu
        35              40


<210>   4
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<212>   PRT
<213>   Homo sapiens


<220>
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<222>   (29)..(29)
<223>   Arg residue is capped with an unsubstituted amide moiety

<400>   4

Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
1               5                  10                    15


Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg
            20                    25


<210>   5
<211>   29
<212>   PRT
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1               5                  10                    15

Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
            20                    25              30


Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu
        35              40


<210>   3
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<212>   PRT
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<220>
<223>   Amino acid sequence of human GRF

<400>   3

Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
1               5                  10                    15


Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
            20                    25              30


Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu
        35              40


<210>   4
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<212>   PRT
<213>   Homo sapiens


<220>
<221>   MISC_FEATURE
<222>   (29)..(29)
<223>   Arg residue is capped with an unsubstituted amide moiety

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Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
1               5                  10                    15


Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg
            20                    25


<210>   5
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<212>   PRT
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<213> Artificial sequence

<220>
<223> Amino acid sequence of minimum active core of human GRF

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Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
1   5   10   15

Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg
            20   25

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<220>
<223> Amino acid sequence corresponding to positions 30 to 44 of human
      GRF

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Gln Gln Gly Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu
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<223> Modified GRF peptide

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<223> Tyr residue is linked to an hexenoyl-trans-3 moiety

<220>
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<222> (44)..(44)
<223> Leu residue is capped with an unsubstituted amide moiety

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Tyr Ala Asp Ala Ile Phe Thr Asn Ser Tyr Arg Lys Val Leu Gly Gln
1   5   10   15

Leu Ser Ala Arg Lys Leu Leu Gln Asp Ile Met Ser Arg Gln Gln Gly
            20   25   30

Glu Ser Asn Gln Glu Arg Gly Ala Arg Ala Arg Leu
            35   40